

1 / 30

CGCGTCCGGGACAGATTACAGTCGTTTCCAGCCAAAGTGACCTGATCGATGGCCCTCCTGAATTTATACAGATATTGAT
TTATTAGCGATGCCCCCTGTTTGTGTGTACGCACACACACAGGTGACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTT
TCCAGCTCCTGGCGAATCCACATCTGTTTCAACTCTCCGCCGAGGCGAGCAGAGTGTCGAATCTGCG
AGTGAAGAGGGACGAGGAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACACAGATC

16
48

M G P P S L V L C L L S A T V F
AGCAAAAAAAGAAG ATG GGC CCC CCG AGC CTC GTG CTG TGC TGC TTG CTG TCC GCA ACT GTG TTC

36
108

S L L G G S S A F L S H H R L K G R F Q
TCC CTG CTG GGT GGA AGC TCG GCC TTC CTG TCG TCG CAC CAC CGC CTG AAA GGC AGG TTT CAG

56
168

R D R R N I R P N I I L V L T D Q D V
AGG GAC CGC AGG AAC ATC CGC CCC AAC ATC ATC CTG GTG CTG ACG GAC GAC CAG GAT GTG

76
228

E L G S M Q V M N K T R R I M E Q G G T
GAG CTG GGT TCC ATG CAG GTG ATG AAC AAC ACC CGG CGC ATC ATG GAG CAG GGC GGC ACG

96
288

H F I N A F V T T P M C C P S R S I L
CAC TTC ATC AAC GCC TTC GTG ACC ACA CCC ATG TGC TGC TGC CCC TCA CGC TCC TCC ATC CTC

116
348

T G K Y V H N H N T Y T N N E N C S S P
ACC GGC AAG TAC GTC CAC AAC CAC AAC ACC TAC ACC AAC AAT GAG AAC TGC TCC TCG CCC

136
408

S W Q A Q H E S R T F A V Y L N S T G Y
TCC TGG CAG GCA CAG CAC GAG AGC CGC ACC TTT GCC GTG TAC CTC AAT AGC ACT GGC TAC

Fig. 1A

2 / 30

CCCCCCCCCCCCCCCC

R	T	A	F	F	G	K	Y	L	N	E	Y	N	G	S	Y	V	P	P	G	156
CGG	ACA	GCT	TTC	TTC	GGG	AAG	TAT	CTT	AAT	GAA	TAC	AAC	GGC	TCC	TAC	GTG	CCA	CCC	GGC	468
W	K	E	W	V	G	L	L	K	N	S	R	F	Y	N	Y	T	L	C	R	176
TGG	AAG	GAG	TGG	GTC	GGA	CTC	CTT	AAA	AAC	TCC	CGC	TTT	TAT	AAC	TAC	ACG	CTG	TGT	CGG	528
N	G	V	K	E	K	H	G	S	D	Y	S	K	D	Y	L	T	D	L	I	196
AAC	GGG	GTG	AAA	GAG	AAG	CAC	GGC	TCC	GAC	TAC	TCC	AAG	GAT	TAC	CTC	ACA	GAC	CTC	ATC	588
T	N	D	S	V	S	F	F	R	T	S	K	K	M	Y	P	H	R	P	V	216
ACC	AAT	GAC	AGC	GTG	AGC	TTC	TTC	CGC	ACG	TCC	AAG	AAG	ATG	TAC	CCG	CAC	AGG	CCA	GTC	648
L	M	V	I	S	H	A	A	P	H	G	P	E	D	S	A	P	Q	Y	S	236
CTC	ATG	GTC	ATC	AGC	CAT	GCA	GCC	CCC	CAC	GGC	CCT	GAG	GAT	TCA	GCC	CCA	CAA	TAT	TCA	708
R	L	F	P	N	A	S	Q	H	I	T	P	S	Y	N	Y	A	P	N	P	256
CGC	CTC	TTC	CCA	AAC	GCA	TCT	CAG	CAC	ATC	ACG	CCG	AGC	TAC	AAC	TAC	GCG	CCC	AAC	CCG	768
D	K	H	W	I	M	R	Y	T	G	P	M	K	P	I	H	M	E	F	T	276
GAC	AAA	CAC	TGG	ATC	ATG	CGC	TAC	ACG	GGG	CCC	ATG	AAG	CCC	ATC	CAC	ATG	GAA	TTC	ACC	828
N	M	L	Q	R	K	R	L	Q	T	L	M	S	V	D	D	S	M	E	T	296
AAC	ATG	CTC	CAG	CGG	AAG	CGC	TTG	CAG	ACC	CTC	ATG	TCG	GTG	GAC	GAC	TCC	ATG	GAG	ACG	888
I	Y	N	M	L	V	E	T	G	E	L	D	N	T	Y	I	V	Y	T	A	316
ATT	TAC	AAC	ATG	CTG	GTT	GAG	ACG	GGC	GAG	CTG	GAC	AAC	ACG	TAC	ATC	GTA	TAC	ACC	GCC	948

Fig. 1B

3 / 30

SECRET

D	H	G	Y	H	I	G	Q	F	G	L	V	K	G	K	S	M	P	Y	E	336
GAC	CAC	GGT	TAC	CAC	ATC	GGC	CAG	TTT	GGC	CTG	GTG	AAA	GGG	AAA	TCC	ATG	CCA	TAT	GAG	1008
F	D	I	R	V	P	F	Y	V	R	G	P	N	V	E	A	G	C	L	N	356
TTT	GAC	ATC	AGG	GTC	CCG	TTC	TAC	GTG	AGG	GGC	CCC	AAC	GTG	GAA	GCC	GGC	TGT	CTG	AAT	1068
P	H	I	V	L	N	I	D	L	A	P	T	I	L	D	I	A	G	L	D	376
CCC	CAC	ATC	GTC	CTC	AAC	ATT	GAC	CTG	GCC	CCC	ACC	ATC	CTG	GAC	ATT	GCA	GGC	CTG	GAC	1128
I	P	A	D	M	D	G	K	S	I	L	K	L	L	D	T	E	R	P	V	396
ATA	CCT	GCG	GAT	ATG	GAC	GGG	AAA	TCC	ATC	CTC	AAG	CTG	CTG	GAC	ACG	GAG	CCG	CCG	GTG	1188
N	R	F	H	L	K	K	K	M	R	V	W	R	D	S	F	L	V	E	R	416
AAT	CGG	TTT	CAC	TTG	AAA	AAG	AAG	ATG	AGG	GTC	TGG	CGG	GAC	TCC	TTC	TTG	GTG	GAG	AGA	1248
G	K	L	L	H	K	R	D	N	D	K	V	D	A	Q	E	E	N	F	L	436
GGC	AAG	CTG	CTA	CAC	AAG	AGA	GAC	AAT	GAC	AAG	GTG	GAC	GCC	CAG	GAG	GAG	AAC	TTT	CTG	1308
P	K	Y	Q	R	V	K	D	L	C	Q	R	A	E	Y	Q	T	A	C	E	456
CCC	AAG	TAC	CAG	CGT	GTG	AAG	GAC	CTG	TGT	CAG	CGT	GCT	GAG	TAC	CAG	ACG	GCG	TGT	GAG	1368
Q	L	G	Q	K	W	Q	C	V	E	D	A	T	G	K	L	K	L	H	K	476
CAG	CTG	GGA	CAG	AAG	TGG	CAG	TGT	GTG	GAG	GAC	GCC	ACG	GGG	AAG	CTG	AAG	CTG	CAT	AAG	1428
C	K	G	P	M	R	L	G	G	S	R	A	L	S	N	L	V	P	K	Y	496
TGC	AAG	GGC	CCC	ATG	CGG	CTG	GGC	GGC	AGC	AGA	GCC	CTC	TCC	AAC	CTC	GTG	CCC	AAG	TAC	1488

Fig. 1C

4 / 30

Sequence 1

Y	G	Q	G	S	E	A	C	T	C	D	S	G	D	Y	K	L	S	L	A	516
TAC	GGG	CAG	GGC	AGC	GAG	GCC	TGC	ACC	TGT	GAC	AGC	GGG	GAC	TAC	AAG	CTC	AGC	CTG	GCC	1548
G	R	R	K	K	L	F	K	K	K	Y	K	A	S	Y	V	R	S	R	S	536
GGA	CGC	CGG	AAA	AAA	CTC	TTC	AAG	AAG	AAG	TAC	AAG	GCC	AGC	TAT	GTC	CGC	AGT	CGC	TCC	1608
I	R	S	V	A	I	E	V	D	G	R	V	Y	H	V	G	L	G	D	A	556
ATC	CGC	TCA	GTG	GCC	ATC	GAG	GTG	GAC	GGC	AGG	GTG	TAC	CAC	GTA	GGC	CTG	GGT	GAT	GCC	1668
A	Q	P	R	N	L	T	K	R	H	W	P	G	A	P	E	D	Q	D	D	576
GCC	CAG	CCC	CGA	AAC	CTC	ACC	AAG	CGG	CAC	TGG	CCA	GGG	GCC	CCT	GAG	GAC	CAA	GAT	GAC	1728
K	D	G	G	D	F	S	G	T	G	G	L	P	D	Y	S	A	A	N	P	596
AAG	GAT	GGT	GGG	GAC	TTC	AGT	GGC	ACT	GGA	GGC	CTT	CCC	GAC	TAC	TCA	GCC	GCC	AAC	CCC	1788
I	K	V	T	H	R	C	Y	I	L	E	N	D	T	V	Q	C	D	L	D	616
ATT	AAA	GTG	ACA	CAT	CGG	TGC	TGC	TAC	ATC	CTA	GAG	AAC	GAC	ACA	GTC	CAG	TGT	GAC	CTG	1848
L	Y	K	S	L	Q	A	W	K	D	H	K	L	L	H	I	D	H	E	I	636
CTG	TAC	AAG	TCC	CTG	CAG	GCC	TGG	AAA	GAC	CAC	AAG	AAG	CTG	CAC	ATC	GAC	CAC	GAG	ATT	1908
T	L	Q	N	K	I	K	N	L	R	E	V	R	G	H	L	K	K	K	R	656
ACC	CTG	CAG	AAC	AAA	ATT	AAG	AAC	CTG	AGG	GAA	GTC	CGA	GGT	CAC	CTG	AAG	AAA	AAG	CGG	1968
P	E	E	C	D	C	H	K	I	S	Y	H	T	Q	H	K	G	R	L	K	676
CCA	GAA	GAA	TGT	GAC	TGT	CAC	AAA	ATC	AGC	TAC	CAC	ACC	CAG	CAC	AAA	GGC	CGC	CTC	AAG	2028

Fig. 1D

[illegible]

H	R	G	S	S	L	H	P	F	R	K	G	L	Q	E	K	D	K	V	W	696
CAC	AGA	GGC	TCC	AGT	CTG	CAT	CCT	TTC	AGG	AAG	GGC	CTG	CAA	GAG	AAG	GAC	AAG	GTG	TGG	2088
L	L	R	E	Q	K	R	K	K	K	L	R	K	L	L	K	R	L	Q	N	716
CTG	TTG	CGG	GAG	CAG	AAG	CGC	AAG	AAG	AAA	CTC	CGC	AAG	CTG	CTC	AAG	CGC	CTG	CAG	AAC	2148
N	D	T	C	S	M	P	G	L	T	C	F	T	H	D	N	Q	H	W	Q	736
AAC	GAC	ACG	TGC	AGC	ATG	CCA	GGC	CTC	ACG	TGC	TTC	ACC	CAC	GAC	AAC	CAG	CAC	TGG	CAG	2208
T	A	P	F	W	T	L	G	P	F	C	A	C	T	S	A	N	N	N	T	756
ACG	GCG	CCT	TTC	TGG	ACA	CTG	GGG	CCT	TTC	TGT	GCC	TGC	ACC	AGC	GCC	AAC	AAT	AAC	ACG	2268
Y	W	C	M	R	T	I	N	E	T	H	N	F	L	F	C	E	F	A	T	776
TAC	TGG	TGC	ATG	AGG	ACC	ATC	AAT	GAG	ACT	CAC	AAT	TTC	CTC	TTC	TGT	GAA	TTT	GCA	ACT	2328
G	F	L	E	Y	F	D	L	N	T	D	P	Y	Q	L	M	N	A	V	N	796
GGC	TTT	CTA	GAG	TAC	TTT	GAT	CTC	AAC	ACA	GAC	CCC	TAC	CAG	CTG	ATG	AAT	GCA	GTG	AAC	2388
T	L	D	R	D	V	L	N	Q	L	H	V	Q	L	M	E	L	R	S	C	816
ACA	CTG	GAC	AGG	GAT	GTC	CTC	AAC	CAG	CTA	CAC	GTA	CAG	CTC	ATG	GAG	CTG	AGG	AGC	TGC	2448
K	G	Y	K	Q	C	N	P	R	T	R	N	M	D	L	G	L	K	D	G	836
AAG	GGT	TAC	AAG	CAG	TGT	AAC	CCC	CGG	ACT	CGA	AAC	ATG	GAC	CTG	GGA	CTT	AAA	GAT	GGA	2508
G	S	Y	E	Q	Y	R	Q	F	Q	R	R	K	W	P	E	M	K	R	P	856
GGA	AGC	TAT	GAG	CAA	TAC	AGG	CAG	TTT	CAG	CGT	CGA	AAG	TGG	CCA	GAA	ATG	AAG	AGA	CCT	2568

Fig. 1E

CGCGT " 26234663

870
2613

S S K S L G Q L W E G W E G *

TCT TCC AAA TCA CTG GGA CAA CTA TGG GAA GGC TGG GAA GGT TAA

GAAACAACAGAGGTGGACCTCCAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGTGATTT
GAAACAACAGAGGTGGACCTCCAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGTGATTT
CCAGCAGACCTGTGCTATTTGGCCAGGAGGCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGA
TAACCCAGCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTTGGCCCTGCTTTTGCTTTGGATTATACCTCACAGCTGC
ACAAAATGCATTTTTCGTATCAAAAAGTCACCACTAACCTTCCCCCAGAACTCACAAAGGAAACCGAGAGAGCGAG
CGAGAGAGATTTCCTTGGAATTTCTCCAAAGGGCGAAAGTCATTTGAAATTTTAAATCATAGGGGAAACGAGTCCCTG
TTCTAAATCCTCTTATTTCTTTGTTTGTACAAAGAGGAACTAAGAAAGCAGGACAGAGGCAACGTGGAGAGGCTGAA
AACAGTGCAGAGACGTTTGACAAATGAGTCAGTAGCACAAAGAGATGACATTTACCTAGCACATAAAACCCCTGGTTGCC
TCTGAAGAAACTGCCTT

Fig. 1F

FOOT 28282600

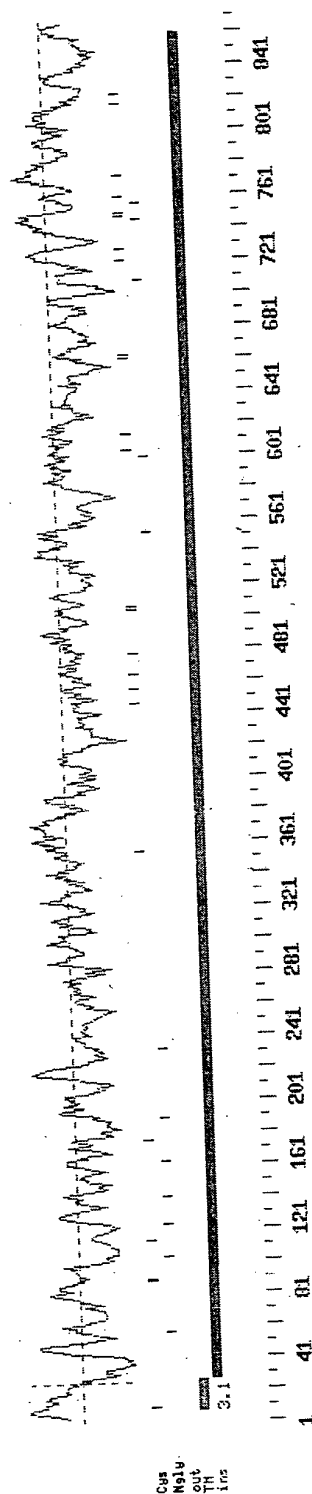


Fig. 2

22437 22437

22437

1247 GAGCGAGAGTGTGTCCGAGTGAGTGTGCGTCTGTGTGTCCCGCGAGGGTGCGCGCTCGGC 60
10 20 30 40 50

22437

1247 GCCGGAGCGCGCCAGCCGAGTCCGGAGGCATCGGGAGTCCGAGAGCCCGCGGACCCC 120
70 80 90 100 110

22437

1247 AGCTCTGCGTTCACTGCCCGCGTCCGGAGCTGGACTTCGGGGCCGGCGCGCGTGC 180
130 140 150 160 170

22437

1247 CCGGGACAGGCAGGGCCGGTCCGGGGCCGGTCCCCAGGCCGAGATCTGCGAGT 240
190 200 210 220 230

Fig. 3A

[illegible]

Fig. 3B

[illegible]

Fig. 3C

22437	CTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAGTATCTTAATGAATACAACGGC	400	410	420	430	440	450
1247	CTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAGTATCTTAATGAATACAACGGC	730	740	750	760	770	780
22437	TCCTACGTGCCACCCGGCTGGAAGAGTGGGTCGGACTCCTTAAAAACTCCCGCTTTTAT	460	470	480	490	500	510
1247	TCCTACGTGCCACCCGGCTGGAAGAGTGGGTCGGACTCCTTAAAAACTCCCGCTTTTAT	790	800	810	820	830	840
22437	AACTACACGCTGTGTCGGAACGGGGTGAAGAGAAAGCAGCGCTCCGACTACTCCAAGGAT	520	530	540	550	560	570
1247	AACTACACGCTGTGTCGGAACGGGGTGAAGAGAAAGCAGCGCTCCGACTACTCCAAGGAT	850	860	870	880	890	900
22437	TACCTCACAGACCTCATCACCAATGACAGCGTGAGCTTCTCCGCACGTCCAAGAAGATG	580	590	600	610	620	630
1247	TACCTCACAGACCTCATCACCAATGACAGCGTGAGCTTCTCCGCACGTCCAAGAAGATG	910	920	930	940	950	960

Fig. 3D

12 / 30

Sequence Alignment

22437	640	650	660	670	680	690
	TACCGCACAGGCCAGTCCTCATGGTCA	TACGCCCATGAGCCCCC	TACGCCCATGAGGCCCTGAGGAT			
1247	970	980	990	1000	1010	1020
	TACCGCACAGGCCAGTCCTCATGGTCA	TACGCCCATGAGGCCCTGAGGAT				
22437	700	710	720	730	740	750
	TCAGCCCCACAATATTCACGCCCTCTTCC	AAACGCAATCTCAGCACATCAGGCCGAGCTAC				
1247	1030	1040	1050	1060	1070	1080
	TCAGCCCCACAATATTCACGCCCTCTTCC	AAACGCAATCTCAGCACATCAGGCCGAGCTAC				
22437	760	770	780	790	800	810
	AACTACGCGCCCAACCCGGACAAACACTGG	ATCATGCGCTACACGGGCCCCATGAAGCCC				
1247	1090	1100	1110	1120	1130	1140
	AACTACGCGCCCAACCCGGACAAACACTGG	ATCATGCGCTACACGGGCCCCATGAAGCCC				
22437	820	830	840	850	860	870
	ATCCACATGGAATTACCAACATGCTCCAGCG	GGAAGCGTTGCAGACCCCTCATGTCGGTG				
1247	1150	1160	1170	1180	1190	1200
	ATCCACATGGAATTACCAACATGCTCCAGCG	GGAAGCGTTGCAGACCCCTCATGTCGGTG				

Fig. 3E

[illegible]

Fig. 3F

FIG. 3G

22437 1120 1130 1140 1150 1160 1170
GACATTGCAGGCCCTGGACATACCTGCGGATATGACGGGAAATCCATCCTCAAGCTGCTG
::: 1180 1190 1200 1210 1220 1230
GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAAGATGAGGGTCTGGCGGGAC
::: 1240 1250 1260 1270 1280 1290
TCCTTCTTGGTGAGAGAGGCAAGCTGTACACAAGAGAGACAATGACAAGGTGGACGCC
::: 1300 1310 1320 1330 1340 1350
CAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAAGCTGTGAG
::: 1360 1370 1380 1390 1400 1410
GACATTGCAGGCCCTGGACATACCTGCGGATATGACGGGAAATCCATCCTCAAGCTGCTG
1420 1430 1440 1450 1460 1470 1480 1490 1500
GACATTGCAGGCCCTGGACATACCTGCGGATATGACGGGAAATCCATCCTCAAGCTGCTG
1510 1520 1530 1540 1550 1560
GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAAGATGAGGGTCTGGCGGGAC
1570 1580 1590 1600 1610 1620
TCCTTCTTGGTGAGAGAGGCAAGCTGTACACAAGAGAGACAATGACAAGGTGGACGCC
22437 1630 1640 1650 1660 1670 1680
CAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAAGCTGTGAG
1247 1690 1700 1710 1720 1730 1740
GACATTGCAGGCCCTGGACATACCTGCGGATATGACGGGAAATCCATCCTCAAGCTGCTG
1750 1760 1770 1780 1790 1800
GACATTGCAGGCCCTGGACATACCTGCGGATATGACGGGAAATCCATCCTCAAGCTGCTG

Fig. 3G

12437	1360	1370	1380	1390	1400	1410
	TACCAGACGGCGTGTGAGCAGCTGGGACAGAAAGTGGCAGTGTGTGGAGGACGCCACGGGG					
	1690	1700	1710	1720	1730	1740
1247	TACCAGACGGCGTGTGAGCAGCTGGGACAGAAAGTGGCAGTGTGTGGAGGACGCCACGGGG					
	1420	1430	1440	1450	1460	1470
22437	AAGCTGAAGCTGCATAAGTGC AAGGGCCCCCATGCGGCTGGGGCGGCAGCAGAGCCCTCTCC					
	1750	1760	1770	1780	1790	1800
1247	AAGCTGAAGCTGCATAAGTGC AAGGGCCCCCATGCGGCTGGGGCGGCAGCAGAGCCCTCTCC					
	1480	1490	1500	1510	1520	1530
22437	AACCTCGTGCCCCAAGTACTACGGGCAGGGCAGCGAGGCCCTGCACCTGTGACAGCGGGGAC					
	1810	1820	1830	1840	1850	1860
1247	AACCTCGTGCCCCAAGTACTACGGGCAGGGCAGCGAGGCCCTGCACCTGTGACAGCGGGGAC					
	1540	1550	1560	1570	1580	1590
22437	TACAAGCTCAGCCTGGCCGGACGCCGGA AAAA AACTCTTCAAGAAAGATACAAGGCCAGC					
	1870	1880	1890	1900	1910	1920
1247	TACAAGCTCAGCCTGGCCGGACGCCGGA AAAA AACTCTTCAAGAAAGATACAAGGCCAGC					

Fig. 3H

22437	1600	1610	1620	1630	1640	1650
	TATGTC	CGCAGT	CGCTCC	ATCCGCTC	AGTGGCCAT	CGAGGTGGACGGCAGGGTGTACCAC
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
	TATGTC	CGCAGT	CGCTCC	ATCCGCTC	AGTGGCCAT	CGAGGTGGACGGCAGGGTGTACCAC
1247	1930	1940	1950	1960	1970	1980
	GTAGG	CCCTGG	GTGATG	CGCGCC	CAGCCCCG	AAACCTCACC
22437	1660	1670	1680	1690	1700	1710
	GTAGG	CCCTGG	GTGATG	CGCGCC	CAGCCCCG	AAACCTCACC
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
	GTAGG	CCCTGG	GTGATG	CGCGCC	CAGCCCCG	AAACCTCACC
1247	1990	2000	2010	2020	2030	2040
	CCTGAG	GACCAAG	ATGAC	AAGGATGG	TGGGGACTT	CAGTGGC
22437	1720	1730	1740	1750	1760	1770
	CCTGAG	GACCAAG	ATGAC	AAGGATGG	TGGGGACTT	CAGTGGC
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
	CCTGAG	GACCAAG	ATGAC	AAGGATGG	TGGGGACTT	CAGTGGC
1247	2050	2060	2070	2080	2090	2100

Fig. 3I

22437	1780	1790	1800	1810	1820	1830
	TACTCAGCCGCCAAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACACA					
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
1247	TACTCAGCCGCCAAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACACA	2110	2120	2130	2140	2150
						2160
	1840	1850	1860	1870	1880	1890
22437	GTCCAGTGTGACCTGGACCTGTACAAAGTCCCTGCAGGCCCTGGAAGACCACACAAGCTGCAC					
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
1247	GTCCAGTGTGACCTGGACCTGTACAAAGTCCCTGCAGGCCCTGGAAGACCACACAAGCTGCAC	2170	2180	2190	2200	2210
						2220
	1900	1910	1920	1930	1940	1950
22437	ATCGACCACGAGATTGAAACCCCTGCAGAAACAAAATTAAAGAACCTGAGGGAAGTCCGAGGT					
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
1247	ATCGACCACGAGATTGAAACCCCTGCAGAAACAAAATTAAAGAACCTGAGGGAAGTCCGAGGT	2230	2240	2250	2260	2270
						2280
	1960	1970	1980	1990	2000	2010
22437	CACCTGAAGAAAAAGCGGCCAGAAAGATGTGACTGTCACAAAATCAGCTACCACACCCAG					
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
1247	CACCTGAAGAAAAAGCGGCCAGAAAGATGTGACTGTCACAAAATCAGCTACCACACCCAG	2290	2300	2310	2320	2330
						2340

Fig. 3J

[illegible]

22437	2020	2030	2040	2050	2060	2070
	CACAAAGCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGCCTGCAA					
	CAAAAGCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGCCTGCAA					
	CAAAAGCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGCCTGCAA					
1247	2350	2360	2370	2380	2390	2400
	2080	2090	2100	2110	2120	2130
22437	GAGAAGGACAAAGTGTGGCTGTTGCGGAGCAGAGCGCAAGAAAGAACTCCGCAAGCTG					
	GAAGGACAAAGTGTGGCTGTTGCGGAGCAGAGCGCAAGAAAGAACTCCGCAAGCTG					
1247	2410	2420	2430	2440	2450	2460
	2140	2150	2160	2170	2180	2190
22437	CTCAAGCGCCTGCAGAACACACACACGTGCAGCATGCCAGGCCTCACGTGCTTCACCCAC					
	CTCAAGCGCCTGCAGAACACACACACGTGCAGCATGCCAGGCCTCACGTGCTTCACCCAC					
1247	2470	2480	2490	2500	2510	2520
	2200	2210	2220	2230	2240	2250
22437	GACAACGACACTGGCAGACGGCGCCTTCTGGACACTGGGGCCTTCTGTGCTGCACACC					
	GACAACGACACTGGCAGACGGCGCCTTCTGGACACTGGGGCCTTCTGTGCTGCACACC					
1247	2530	2540	2550	2560	2570	2580

Fig. 3K

22437 22437 22437

```
22437 2260 2270 2280 2290 2300 2310
AGGCCAACAATAACACGTACTGGTGCAATGAGGACCATCAATGAGACTCACAATTTCCTC
:::
1247 2590 2600 2610 2620 2630 2640
AGGCCAACAATAACACGTACTGGTGCAATGAGGACCATCAATGAGACTCACAATTTCCTC
:::
22437 2320 2330 2340 2350 2360 2370
TTCTGTGAATTTGCAACTGGCTTCCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG
:::
1247 2650 2660 2670 2680 2690 2700
TTCTGTGAATTTGCAACTGGCTTCCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG
:::
22437 2380 2390 2400 2410 2420 2430
CTGATGAATGCAGTGAACACACACTGGACAGGGATGTCCCTCAACCAGCTACACGTACAGCTC
:::
1247 2710 2720 2730 2740 2750 2760
CTGATGAATGCAGTGAACACACACTGGACAGGGATGTCCCTCAACCAGCTACACGTACAGCTC
:::
22437 2440 2450 2460 2470 2480 2490
ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCGGACTCGAAACATGGAC
:::
1247 2770 2780 2790 2800 2810 2820
ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCGGACTCGAAACATGGAC
:::
```

Fig. 3L

[illegible]

2050

2560 2570 2580 2590 2600 2610

CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGACAACACTGTGGGAAGGCTGGGAAGGT

22437

2560 2570 2580 2590 2600 2610

CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGACAACACTGTGGGAAGGCTGGGAAGGT

1247

2890 2900 2910 2920 2930 2940

CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGACAACACTGTGGGAAGGCTGGGAAGGT

22437

1247
TGAAAACCATGTGGTGATTCCAGCAGACCTGTGCTATTGCCAGGAGGCTGAGAAA
3010 3020 3030 3040 3050 3060

Fig. 3M

DATE	DESCRIPTION	AMOUNT	BALANCE
1941			
1942			
1943			
1944			
1945			
1946			
1947			
1948			
1949			
1950			
1951			
1952			
1953			
1954			
1955			
1956			
1957			
1958			
1959			
1960			
1961			
1962			
1963			
1964			
1965			
1966			
1967			
1968			
1969			
1970			
1971			
1972			
1973			
1974			
1975			
1976			
1977			
1978			
1979			
1980			
1981			
1982			
1983			
1984			
1985			
1986			
1987			
1988			
1989			
1990			
1991			
1992			
1993			
1994			
1995			
1996			
1997			
1998			
1999			
2000			
2001			
2002			
2003			
2004			
2005			
2006			
2007			
2008			
2009			
2010			
2011			
2012			
2013			
2014			
2015			
2016			
2017			
2018			
2019			
2020			
2021			
2022			
2023			
2024			
2025			
2026			
2027			
2028			
2029			
2030			
2031			
2032			
2033			
2034			
2035			
2036			
2037			
2038			
2039			
2040			
2041			
2042			
2043			
2044			
2045			
2046			
2047			
2048			
2049			
2050			
2051			
2052			
2053			
2054			
2055			
2056			
2057			
2058			
2059			
2060			
2061			
2062			
2063			
2064			
2065			
2066			
2067			

22437

1247

GCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGA
3070 3080 3090 3100 3110 3120

22437

1247

TAACCTCAGGAAGTCCATTTTGGCCCCTGCTTTTGGATTATACCTCACCAGCTGC 3130 3140 3150 3160 3170 3180

22437

1247

ACAAAATGCATTTTTTCGTATCAAAAAGTCACCACTAACCCCTCCCCCAGAAAGCTCACAAA
3190 3200 3210 3220 3230 3240

22437

1247

GGAAAACGGAGAGCGGAGAGAGATTCTTGAAATTTCTCCCAAGGCGAAAGT 3300

Fig. 3N

Sequence 22437

22437

1247 CATTGGAATTTTAAATCATAGGGGAAAGCAGTCCTGTTCTTAAATCCTTATTCCTTT 3360
3310 3320 3330 3340 3350

22437
GGTTGTCACAAAGAAAGGAACTAAGAAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAAC 3420
3370 3380 3390 3400 3410

22437
1247 AGTGCAGAGACGTTTGACAAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACT 3480
3430 3440 3450 3460 3470

22437
1247 ATAAACCCCTGGTTGCCCTCTGAAGAAACTGCCCTTCATTGTATATATGTGACTATTTACATG 3540
3490 3500 3510 3520 3530

Fig. 30

22437 22437 22437

22437
1247
3550 3560 3570 3580 3590 3600
TAATCAACATGGGAACCTTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTG

22437
1247
3610 3620 3630 3640 3650 3660
GTGTCAATAACGCTCTGTGGCCAGTGTAAGAAATCCCTCGCAGTTGTGGACATTC

22437
1247
3670 3680 3690 3700 3710 3720
TGTTCCCTGCCAGATACCATTTCTCCTAGTATTTCTTTGTTATGTCGCCAGAACTGATGTT

22437
1247
3730 3740 3750 3760 3770 3780
TTTTTTTAAAGGTACTGAAAAGAAATGAAAGTTGATGTATGTCCCAAGTTTGTGATGAAACT

Fig. 3P

GGGTTT 2326666

22437

1247 GTATTGTAAATAATTTGTAGTTTAAAGTATGTCATACAGTGTCAAAACCCAGCC 3840
3790 3800 3810 3820 3830

22437
1247 AATGACCAGCAGTTGGTATGAAGAACCCTTGACATTTTGTAAGGCCATTCTCTTCTTG 3900
3850 3860 3870 3880 3890

22437
1247 GGAGTTTTTGGTGTCTGTTTTTTTAAAGTATCAAGATACTACCAGTCAACATCTTT 3960
3910 3920 3930 3940 3950

22437
1247 TTGGAAGAAAATGCCCTTGGGTTTGAAGATTTTCTTAAAGGGGAGTAGATGGTTGTAGA 4020
3970 3980 3990 4000 4010

Fig. 3Q

SEQUENCE 23232600

```
-----  
22437  
1247 TTGACTAAAAAGTCTACCATACTTCAAGGGACTACAGGTAAGTCTCATAGTATACCAGCT 4080  
4030 4040 4050 4060 4070  
-----  
22437  
1247 TTGGTACTTCATTTTTTAAAAAAGTATTAATCAATTGCAAAGAAATTCGCCCTTGGCCAAAC 4140  
4090 4100 4110 4120 4130  
-----  
22437  
1247 CCTTCTTTGTGTATCAGGTAGTCTAACCTGATACAAGTAGTTGACAGATTTCAACTATCA 4200  
4150 4160 4170 4180 4190  
-----  
22437  
1247 ATCACCAGTCCAACCCATTCTCTCATTTAACAGATGACGGAGATAATCCCTAAAGCACCCC 4260  
4210 4220 4230 4240 4250
```

Fig. 3R

4320 4310 4300 4290 4280 4270

22437
1247
ACATTGTTCATGCCCCCAACAGGCCAAGGCTCCCTAGCAACTCCCCTAGTGGCGTTTT
4270 4280 4290 4300 4310 4320

22437
1247
TTAACTTCTCAGAAACTGTTACCATTTATTGAAAATAGGCTTCCTTAACCTCCTTTACCCCT
4330 4340 4350 4360 4370 4380

22437
1247
TAACCCCAACAGGGATT
4390

Fig. 3S

22437	-----MGPPSLVCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPN	10	20	30	40
1247	DSRIPKEAPDQKKMGPPSLVCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPN	10	20	30	40
22437	IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTMCCPSRSSILTGKYVHNHN	50	60	70	80
1247	IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTMCCPSRSSILTGKYVHNHN	70	80	90	100
22437	TYTNNENCSSPSWQAQHESTRFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLK	110	120	130	140
1247	TYTNNENCSSPSWQAQHESTRFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLK	130	140	150	160
22437	NSRFYNYTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAP	170	180	190	200
1247	NSRFYNYTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAP	190	200	210	220

Fig. 4A

22437 1247

```
230      240      250      260      270      280
HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQ
:::
HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQ
250      260      270      280      290      300
HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQ
290      300      310      320      330      340
TLMSVDDSMETIYNMLVETGELDNITYIVYTADHGYPHIGQFGLVKGKSMPEFFDIRVPFYV
:::
TLMSVDDSMETIYNMLVETGELDNITYIVYTADHGYPHIGQFGLVKGKSMPEFFDIRVPFYV
310      320      330      340      350      360
TLMSVDDSMETIYNMLVETGELDNITYIVYTADHGYPHIGQFGLVKGKSMPEFFDIRVPFYV
350      360      370      380      390      400
RGPVNEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKM
:::
RGPVNEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKM
370      380      390      400      410      420
RGPVNEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKM
410      420      430      440      450      460
RVWRDSFLVERGKLLHKRDNDKVDQAEEENFLPKYQVRVKDLCCQRAEYQTACEQLGQKWQCV
:::
RVWRDSFLVERGKLLHKRDNDKVDQAEEENFLPKYQVRVKDLCCQRAEYQTACEQLGQKWQCV
430      440      450      460      470      480
RVWRDSFLVERGKLLHKRDNDKVDQAEEENFLPKYQVRVKDLCCQRAEYQTACEQLGQKWQCV
```

Fig. 4B

[illegible]

Fig. 4C

Figure 4D

	710	720	730	740	750	760
22437	KLRKLLKRLQNNDTC	SMPLTCT	HDNQHWQT	APFWTL	GPFC	ACTSANNNTYWC
	770	780	790	800	810	820
1247	THNFL	CE	FATG	FLEY	FDLNTD	PYQLMNAVNTLDRDVLNQ
	830	840	850	860	870	880
22437	TRNMDL	GLK	DGGS	YEYRQ	FQRRKWP	EMKRPSSKSLGQLWEG
1247	TRNMDL	GLK	DGGS	YEYRQ	FQRRKWP	EMKRPSSKSLGQLWEG

Fig. 4D